



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/836,911
Source: O/PE
Date Processed by STIC: 5/3/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

BEST AVAILABLE COPY

QIPE

RAW SEQUENCE LISTING DATE: 05/03/2001
PATENT APPLICATION: US/09/836,911 TIME: 15:56:14

Input Set : A:\402iseq.001
Output Set: N:\CRF3\05032001\I836911.raw

Does Not Comply
Corrected Diskette Needed

SEQUENCE LISTING

C--> 4 (1) GENERAL INFORMATION:
6 (i) APPLICANT: Hadlaczky, Gyula
7 Szalay, Aladar
C--> 9 (ii) TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF
10 AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES
12 (iii) NUMBER OF SEQUENCES: 34
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: Heller Ehrman White & McAuliffe
16 (B) STREET: 4350 La Jolla Village Drive, 6th Floor
17 (C) CITY: San Diego
18 (D) STATE: CA
19 (E) COUNTRY: USA
20 (F) ZIP: 92122
22 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: Diskette
24 (B) COMPUTER: IBM Compatible
25 (C) OPERATING SYSTEM: DOS
26 (D) SOFTWARE: FastSEQ Version 1.5
28 (vi) CURRENT APPLICATION DATA:
C--> 29 (A) APPLICATION NUMBER: US/09/836,911
C--> 30 (B) FILING DATE: 17-Apr-2001
50 (C) CLASSIFICATION:
C--> 47 (vii) PRIOR APPLICATION DATA:
33 (A) APPLICATION NUMBER: 08/835,682
34 (B) FILING DATE: 10-APR-1997
38 (A) APPLICATION NUMBER: 08/695,191
39 (B) FILING DATE: 07-AUG-1996
43 (A) APPLICATION NUMBER: 08/682,080
44 (B) FILING DATE: 15-JUL-1996
48 (A) APPLICATION NUMBER: 08/629,822
49 (B) FILING DATE: 10-APR-1996
52 (viii) ATTORNEY/AGENT INFORMATION:
53 (A) NAME: Seidman, Stephanie L
54 (B) REGISTRATION NUMBER: 33,779
55 (C) REFERENCE/DOCKET NUMBER: 24601-402I
58 (ix) TELECOMMUNICATION INFORMATION:
59 (A) TELEPHONE: 858-450-8403
60 (B) TELEFAX: 858-587-5360
61 (C) TELEX:
63 (2) INFORMATION FOR SEQ ID NO: 1:
65 (i) SEQUENCE CHARACTERISTICS:
66 (A) LENGTH: 1293 base pairs
67 (B) TYPE: nucleic acid
68 (C) STRANDEDNESS: single
69 (D) TOPOLOGY: linear
71 (ii) MOLECULE TYPE: Genomic DNA

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72 (iii) HYPOTHETICAL: NO
C--> 73 (iv) ANTI-SENSE: NO
W--> 74 (v) FRAGMENT TYPE:
75 (vi) ORIGINAL SOURCE:
76 (ix) FEATURE:
78 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
80 GAATTCCATCA TTTTTCANGT CCTCAAGTGG ATGTTTCTCA TTTNCCATGA TTTTAAGTTT 60
81 TCTCGCCATA TTCCTGGTCC TACAGTGTGC ATTTCTCCAT TTTNCACGTT TTNCAGTGAT 120
82 TTCTGCATTT TCAAGTCCTC AAGTGGATGT TTCTCATTN CCATGAATTT CAGTTTCTN 180
83 GCCATATTCC ACGTCCCTACA GNGGACATTT CAAATTTNC CACCTTTTC AGTTTCTCCTC 240
84 GCCATATTTC ACGTCCCTAA ATGTTGATTT CTGCTTNC GTGATTTCA GTTTCTCGC 300
85 CAGATTCCAG GTCCTATAAT GTGCATTCTC CATTNNAC CTTTTCAGT GATTCGTCA 360
86 TTTTTCAAG TCGGAAGTG GATGTTCTC ATTTNCCATG ATTTNCAGTT TTCTTGNAA 420
87 ATTCATGTC CTACAATGAT CATTNTTAAT TTTCCACCTT TTCATTTC CAGCCATAT 480
88 TTCATGTCCT AAAGTGTATA TTTCTCCCTT TCCGCGATTTC AGTTTCTCT CGCCATATTC 540
89 CAGGTCTAC AGTGTGCATT CCTCATTTC CACCTTTTC ACTGATTCG TCATTTC 600
90 AGTCGTCAAC TGGATCTTC TAATTTCGA TGATTTTCAG TTATCTGTC ATATTCCATG 660
91 TCCTACAGTG GACATTCTA AATTTCCTAA CTTTTCAAT TTTCTCGAC ATATTGACG 720
92 TGCTAAAGTG TGTATTCTT ATTTCCTGTG ATTTTCAGTT TTCTCGCCAT ATTCCAGGTC 780
93 CTAATAGTGT GCATTTCTCA TTTTCACGT TTTTCAGTGA TTTCGTCTT TTTCCAGTT 840
94 GTCAAGGGGA TGTTTCTCAT TTTCCATGAG TGTCAGTTTT CTTGCTATAT TCCATGTCCT 900
95 ACAGTGACAT TTCTAAATAT TATACCTTT TCAGTTTTTC TCACCATATT TCACGTCTA 960
96 AAGTATATAT TTCTCATTTC CCCTGATTTT CAGTTTCCCTT GCCATATTCC AGGTCCCTACA 1020
97 GTGTGCATTTC CTCATTTC ACGTTTTCA GAAATTCTT CATTTCCTAA GCCTCAAAT 1080
98 GGATGTTCTC CATTTCAT GATTTTCAGT TTCTTGCCA TATACCATGT CCTACAGTGG 1140
99 ACATTTCTAA ATTATCCACC TTTTCAGTT TTTCATCGGC ACATTTCACG TCCTAAAGTG 1200
100 TGTATTCTA ATTTCAGTG ATTTTCAGTT TTCTCGCCAT ATTCCAGGAC CTACAGTGTG 1260
101 CATTTCAT TTTTCACGTT TTTCAGTGAA TTC 1293
103 (2) INFORMATION FOR SEQ ID NO: 2:
105 (i) SEQUENCE CHARACTERISTICS:
106 (A) LENGTH: 1044 base pairs
107 (B) TYPE: nucleic acid
108 (C) STRANDEDNESS: single
109 (D) TOPOLOGY: linear
111 (ii) MOLECULE TYPE: Genomic DNA
112 (iii) HYPOTHETICAL: NO
C--> 113 (iv) ANTI-SENSE: NO
W--> 114 (v) FRAGMENT TYPE:
115 (vi) ORIGINAL SOURCE:
116 (ix) FEATURE:
118 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
120 AGGCCTATGG TGAAAAAGGA AATATCTTCC CCTGAAACT AGACAGAAGG ATTCTCAGAA 60
121 TCTTATTGATGTCGCGCC CCTCAACTAA CAGTGTGAA GCTTTCTTT GATAGAGCAG 120
122 TTTTGAAACA CTCTTTGATGCA AAAATCTGCA AGAGGATATT TGGATAGCTT TGAGGATTTC 180
123 CGTTGGAAAC GGGATTGTCT TCATATAAAC CCTAGACAGA AGCATTCTCA GAAGCTTCAT 240
124 TGGGATGTTT CAGTTGAAGT CACAGTGTG AACAGTCCCC TTTCATAGAG CAGGTTTGAA 300
125 ACACCTTTT TTGTAGTATC TGGAAAGTGG AATTTGGAGC GATCTCAGGA CTGCGGTGAA 360
126 AAAGGAAATA TCTTCCAATA AAAGCTAGAT AGAGGCAATG TCAGAAACCT TTTTCATGAT 420
127 GTATCTACTC AGCTAACAGA GTTGAACCTT CCTTGAGAG AGCAGTTTG AAACACTCTT 480

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128	TTTGTGGAAT	CTGCAAGTGG	ATATTGTCT	AGCTTGGAGG	ATTCGTTGG	GAAACGGGAT	540
129	TACATATAAA	AAGCAGACAG	CAGCATTCCC	AGAAACTTCT	TTGTGATGTT	TGCATTCAAG	600
130	TCACAGAGTT	GAACATTCCC	TTTCATAGAG	CAGGTTTGA	ACACACTTTT	TGATGTATCT	660
131	GGATGTGGAC	ATTTGCAGCG	CTTCAGGCC	TAAGGTGAAA	AGGAAATATC	TCCCCCTGAA	720
132	AACTAGACAG	AAGCATTCTC	AGAAACTTAT	TTGTGATGTT	CGCCCTCAAC	TAACAGTGT	780
133	GAAGCTTCT	TTTGATAGAG	GCAGTTTGA	AACACTCTT	TGTGGATCT	GCAAGTGGAT	840
134	ATTGTCTAG	CTTTGAGGAT	TTCTTGGAA	ACGGGATTAC	ATATAAAAG	CAGACAGCAG	900
135	CATTCCCAGA	ATCTTGTGTTG	TGATGTTGC	ATTCAAGTCA	CAGAGTTGAA	CATTCCCTTT	960
136	CAGAGAGCAG	GTGGAAACAC	TCTTTTATA	GTATCTGGAT	GTGGACATTT	GGAGCGCTTT	1020
137	CAGGGGGGAT	CCTCTAGAAT	TCCT				1044

141 (2) INFORMATION FOR SEQ ID NO: 3:

143 (i) SEQUENCE CHARACTERISTICS:

144 (A) LENGTH: 2492 base pairs

145 (B) TYPE: nucleic acid

146 (C) STRANDEDNESS: single

147 (D) TOPOLOGY: linear

149 (ii) MOLECULE TYPE: Genomic DNA

150 (iii) HYPOTHETICAL: NO

C--> 151 (iv) ANTI-SENSE: NO

W--> 152 (v) FRAGMENT TYPE:

153 (vi) ORIGINAL SOURCE:

154 (ix) FEATURE:

156 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

158	CTGCAGCTGG	GGGTCTCCAA	TCAGGCAGGG	GCCCCTACT	ACTCAGATGG	GGTGGCCGAG	60
159	TAGGGGAAGG	GGGTGCCAGGC	TCCATGAGTG	GACACAGCTG	TAGGACTACC	TGGGGGCTGT	120
160	GGATCTATGG	GGGTGGGAG	AAGCCCAGTG	ACAGTGCCTA	GAAGAGACAA	GGTGGCCTGA	180
161	GAGGGTCTGA	GGAACATAGA	GCTGGCCATG	TTGGGGCCAG	GTCTCAAGCA	GGAAGTGAGG	240
162	AATGGGACAG	GCTTGAGGAT	ACTCTACTCA	GTAGCCAGGA	TAGCAAGGAG	GGCTTGGGGT	300
163	TGCTATCTG	GGGTTCAACC	CCCCAGGTTG	AAGGCCCTGG	GGGAGATGGT	CCCAGGACAT	360
164	ATTACAATGG	ACACAGGAGG	TTGGGACACC	TGGAGTCACC	AAACAAAACC	ATGCCAAGAG	420
165	AGACCATGAG	TAGGGGTGTC	CAGTCCAGCC	CTCTGACTGA	GCTGCATTGT	TCAAATCCAA	480
166	AGGGCCCTG	CTGCCACCTA	GTGGCTGATG	GCATCCACAT	GACCCTGGC	CACACGCGTT	540
167	TAGGGTCTCT	GTGAAGACCA	AGATCCTTGT	TACATTGAAC	GACTCCTAAA	TGAGCAGAGA	600
168	TTTCCACCTA	TCGAAACAA	TCACATAAAA	TCCATCCTGG	AAAAAGCCTG	GGGGATGGCA	660
169	CTAAGGCTAG	GGATAGGGTG	GGATGAAGAT	TATAGTTACA	GTAAGGGTT	TAGGGTTAGG	720
170	GATCAACGTT	GGTTAGGGT	TAGGGATACA	GTAGGGTACC	GGTAGGGTTA	GGGGTTAGGG	780
171	TTAGGGGTTA	GGGTTAGGGT	TAGGGTTAGG	GTTAGGGTTA	GGGGTTAGGG	GTAGGGTTA	840
172	GGGTTAGGGT	TTGGGGTGGC	GTATTTGGT	CTTATACGCT	GTGTCCTCACT	GGCAATGAAA	900
173	AGAGTTCTTG	TTTTCTCTC	AGCAATTGT	CATTTTAAA	AGAGTTTACG	AATTCTAAC	960
174	GATATAGACC	AGCTGTGCTA	TCTCATTGTC	GTGTTCAATT	GTAACCACAT	TGTGGTTCA	1020
175	ATGTGTTAC	TTGCCATCTG	TAGATCTCT	TTGCGTGAGG	TGTCTGTTCA	GATGTGTGT	1080
176	CATTCTTGN	NTTNGGCTG	TTTAACATTAT	TGTTTAGTT	TAATAATTTC	TTATATATT	1140
177	GAAGACAAAT	CTTCTCAGA	TGTGATTTC	CAAATATTTC	TTCAATATGA	GGCTTGCTTT	1200
178	TGTCTCAAC	AAGGTCTTT	CAGAGATAAC	TTAAATATAA	GAAATCCACA	CTGTCACTTC	1260
179	TTTGTTGTAT	ATCTACCTT	TGTGTCATT	GTAAAATTTC	ATTACCAAC	CCAAAGGCAG	1320
180	ATAGCTTTTC	TTCTATTGTT	TCTTCTAGAA	ATTTGTATAG	TTTGCAATT	TTAGTGTAAAG	1380
181	GATGATTTTG	AGTGATTATT	TGTGTAAGTT	GTAAAGTTT	CGTCTATATC	CATATCATT	1440
182	CTTATGGTTT	CCAATTAAATC	GTTCCTCAC	TATTTTGGG	AAAGACACAG	GATAGTGGGC	1500
183	TTTGTAGAG	TAGATAGGTA	GCTAGACATG	ACACGGAGGG	GGCCTCCTGG	AAAAGGGAAA	1560

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184	GCTCTGGGAAG	GCTCACCTGG	AGGACCACCA	AAAATTACA	TATTAGTAGC	ATCTCTAGTG	1620
185	CTGGAGTGG	TGGGCACTTG	TCAATTGTGG	GTAGGAGGGA	AAAGAGGTCC	TATGCAGAAA	1680
186	GAAACTCCCT	AGAACTCCTC	TGAAGATGCC	CCAATCATTC	ACTCTGCAAT	AAAAATGTCA	1740
187	GAATATTGCT	AGCTACATGC	TGATAAGGNN	AAAGGGGACA	TTCTTAAGTG	AAACCTGGCA	1800
188	CCATAAGTAC	AGATTAGGGC	AGAGAAGGAC	ATTCAAAAGA	GGCAGCGCA	GTAGGTACAA	1860
189	ACGTGATCGC	TGTCAGTGTG	CCTGGGATGG	CGGGAAGGAG	GCTGGTGCCA	GAGTGGATTG	1920
190	GTATTGATCA	CCACACATAT	ACCTCAACCA	ACAGTGAGGA	GGTCCACAA	GCCTAAGTGG	1980
191	GGCAAGTTGG	GGAGCTAAGG	CAGTAGCAGG	AAAACCAGAC	AAAGAAAACA	GGTGGAGACT	2040
192	TGAGACAGAG	GCAGGAATGT	GAAGAAATCC	AAAATAAAAT	TCCCTGCACA	GGACTCTTAG	2100
193	GCTGTTAAT	GCATCGCTCA	GTCCCACCTCC	TCCCTATTGTT	TCTACAATAA	ACTCTTTACA	2160
194	CTGTGTTTCT	TTTCAATGAA	GTATCTGCC	ATCTTTGTAT	TGCCTCTTGG	TGAAAATGTT	2220
195	TCTTCCAAGT	TAAACAAGAA	CTGGGACATC	AGCTCTCCC	AGTAATAGCT	CCGTTTCAGT	2280
196	TTGAATTAC	AGAACTGATG	CGCTTAATAA	CTGGCGCTCT	GACTTTAGTG	GTGCAGGAGG	2340
197	CCGTACACCC	GGGACCAAGA	GTGCCCTGCC	TAGTCCCCAT	CTGCCCGCAG	GTGGCGGCTG	2400
198	CCTCGACACT	GACAGCAATA	GGGTCCGGCA	GTGTCCCCAG	CTGCCAGCAG	GGGGCGTACG	2460
199	ACGACTACAC	TGTGAGCAAG	AGGGCCCTGC	AG			2492

201 (2) INFORMATION FOR SEQ ID NO: 4:
 203 (i) SEQUENCE CHARACTERISTICS:
 204 (A) LENGTH: 28 base pairs
 205 (B) TYPE: nucleic acid
 206 (C) STRANDEDNESS: single
 207 (D) TOPOLOGY: linear
 209 (ii) MOLECULE TYPE: Genomic DNA
 210 (iii) HYPOTHETICAL: NO
 C--> 211 (iv) ANTI-SENSE: NO
 W--> 212 (v) FRAGMENT TYPE:
 213 (vi) ORIGINAL SOURCE:
 214 (ix) FEATURE:
 216 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 218 GGGGAATTCA TTGGGATGTT TCAGTTGA

28

220 (2) INFORMATION FOR SEQ ID NO: 5:
 222 (i) SEQUENCE CHARACTERISTICS:
 223 (A) LENGTH: 29 base pairs
 224 (B) TYPE: nucleic acid
 225 (C) STRANDEDNESS: single
 226 (D) TOPOLOGY: linear
 228 (ii) MOLECULE TYPE: Genomic DNA
 229 (iii) HYPOTHETICAL: NO
 C--> 230 (iv) ANTI-SENSE: NO
 W--> 231 (v) FRAGMENT TYPE:
 232 (vi) ORIGINAL SOURCE:
 233 (ix) FEATURE:
 235 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 237 CGAAAGTCCC CCCTAGGAGA TCTTAAGGA

29

239 (2) INFORMATION FOR SEQ ID NO: 6:
 241 (i) SEQUENCE CHARACTERISTICS:
 242 (A) LENGTH: 47 base pairs
 243 (B) TYPE: nucleic acid
 244 (C) STRANDEDNESS: single

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/836,911

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Input Set : A:\402iseg.001
Output Set: N:\CRF3\05032001\I836911.raw

245 (D) TOPOLOGY: linear
W--> 247 (ii) MOLECULE TYPE: DNA
248 (iii) HYPOTHETICAL: NO
C--> 249 (iv) ANTI-SENSE: NO
W--> 250 (v) FRAGMENT TYPE:
251 (vi) ORIGINAL SOURCE:
252 (ix) FEATURE:
254 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
256 CCGCTTAATA CTCTGATGAG TCCGTGAGGA CGAAACGCTC TCGCACC
260 (2) INFORMATION FOR SEQ ID NO: 7: 47
262 (i) SEQUENCE CHARACTERISTICS:
263 (A) LENGTH: 25 base pairs
264 (B) TYPE: nucleic acid
265 (C) STRANDEDNESS: single
266 (D) TOPOLOGY: linear
268 (ii) MOLECULE TYPE: Genomic DNA
269 (iii) HYPOTHETICAL: NO
C--> 270 (iv) ANTI-SENSE: NO
W--> 271 (v) FRAGMENT TYPE:
272 (vi) ORIGINAL SOURCE:
273 (ix) FEATURE:
275 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
277 CGATTAAAT TAATTAAGCC CGGGC
280 (2) INFORMATION FOR SEQ ID NO: 8: 25
282 (i) SEQUENCE CHARACTERISTICS:
283 (A) LENGTH: 27 base pairs
284 (B) TYPE: nucleic acid
285 (C) STRANDEDNESS: single
286 (D) TOPOLOGY: linear
288 (ii) MOLECULE TYPE: Genomic DNA
289 (iii) HYPOTHETICAL: NO
C--> 290 (iv) ANTI-SENSE: NO
W--> 291 (v) FRAGMENT TYPE:
292 (vi) ORIGINAL SOURCE:
293 (ix) FEATURE:
295 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
297 TAAATTAAAT TAATTGGGC CCGTCGA
299 (2) INFORMATION FOR SEQ ID NO: 9: 27
301 (i) SEQUENCE CHARACTERISTICS:
302 (A) LENGTH: 69 base pairs
303 (B) TYPE: nucleic acid
304 (C) STRANDEDNESS: single
305 (D) TOPOLOGY: linear
307 (ii) MOLECULE TYPE: Genomic DNA
310 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
312 ATG TAC AGG ATG CAA CTC CTG TCT TGC ATT GCA CTA AGT CTT GCA CTT 48
313 Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
W--> 315 GTC ACA AAC AGT GCA CCT ACT 69
316 Val Thr Asn Ser Ala Pro Thr

(Per
Sequence Rules)

→ Number

→ the
amino
acids

under every
5 amino
acids — do not
use TAB codes
between numbers 5/3/01

Please edit all subsequent sequences
containing these errors

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/836,911

DATE: 05/03/2001

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Input Set : A:\402iseg.001

Output Set: N:\CRF3\05032001\I836911.raw

L:4 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:9 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:37 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:42 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:47 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:73 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:78 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=1
L:74 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=1
L:113 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:118 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=2
L:114 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=2
L:151 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:156 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=3
L:152 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=3
L:211 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:216 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=4
L:212 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=4
L:230 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:235 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=5
L:231 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=5
L:249 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:254 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=6
L:247 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6
L:250 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=6
L:270 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:275 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=7
L:271 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=7
L:290 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:295 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=8
L:291 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=8
L:308 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]
L:308 M:220 C: Keyword misspelled or invalid format, Poss data loss, Seq 9, (D) OTHER INFORMATION:
L:315 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:339 M:220 C: Keyword misspelled or invalid format, [(H) DOCUMENT NUMBER:]
L:433 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:438 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=11
L:434 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=11
L:452 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:457 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=12
L:453 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=12
L:471 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:472 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=13
L:512 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:513 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=14
L:553 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:554 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=15

VERIFICATION SUMMARY

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L:593 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:594 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=16
L:979 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:980 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=17
L:1713 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1714 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=18
L:1734 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1735 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=19
L:1764 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1765 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=20
L:1789 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1790 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=21
L:1813 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1814 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=22
L:1837 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1838 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=23
L:1866 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1867 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=24
L:1896 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1897 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=25
L:1914 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1915 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=26
L:1932 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1933 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=27
L:1950 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1951 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=28
L:1968 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1969 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=29
L:1987 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1988 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=30
L:2005 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2006 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=31
L:2023 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2024 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=32
L:2041 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2042 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=33
L:2059 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2060 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=34